RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: _____ 10/525,535

Source: _____ IFW16

Date Processed by STIC: _____ 03/08/2007

ENTERED

IFW16

```
 4 <110> APPLICANT: Wong, Justin
 5        Winter, Jill
 6        Lalehzadeh, Guita
 7        Warne, Robert
 9 <120> TITLE OF INVENTION: Compositions and Methods of Therapy for
10        Cancers Characterized by Expression of the Tumor-Associated
11        Antigen MN/CA IX
13 <130> FILE REFERENCE: PP019155.0004
15 <140> CURRENT APPLICATION NUMBER: US 10/525,535
16 <141> CURRENT FILING DATE: 2005-02-23
18 <150> PRIOR APPLICATION NUMBER: PCT/US2003/026612
19 <151> PRIOR FILING DATE: 2003-08-25
21 <150> PRIOR APPLICATION NUMBER: 60/405,577
22 <151> PRIOR FILING DATE: 2002-08-23
24 <160> NUMBER OF SEQ ID NOS: 10
26 <170> SOFTWARE: FastSEQ for Windows Version 4.0
28 <210> SEQ ID NO: 1
29 <211> LENGTH: 1380
30 <212> TYPE: DNA
31 <213> ORGANISM: Homo sapiens
33 <220> FEATURE:
34 <221> NAME/KEY: CDS
35 <222> LOCATION: (1)...(1380)
37 <400> SEQUENCE: 1
38 atg gct ccc ctg tgc ccc agc ccc tgg ctc cct ctg ttg atc ccg gcc    48
39 Met Ala Pro Leu Cys Pro Ser Pro Trp Leu Pro Leu Leu Ile Pro Ala
40  1               5                  10                  15
42 cct gct cca ggc ctc act gtg caa ctg ctg ctg tca ctg ctg ctt ctg    96
43 Pro Ala Pro Gly Leu Thr Val Gln Leu Leu Leu Ser Leu Leu Leu Leu
44              20                  25                  30
46 atg cct gtc cat ccc cag agg ttg ccc cgg atg cag gag gat tcc ccc   144
47 Met Pro Val His Pro Gln Arg Leu Pro Arg Met Gln Glu Asp Ser Pro
48              35                  40                  45
50 ttg gga gga ggc tct tct ggg gaa gat gac cca ctg ggc gag gag gat   192
51 Leu Gly Gly Gly Ser Ser Gly Glu Asp Asp Pro Leu Gly Glu Glu Asp
52          50                  55                  60
54 ctg ccc agt gaa gag gat tca ccc aga gag gag gat cca ccc gga gag   240
55 Leu Pro Ser Glu Glu Asp Ser Pro Arg Glu Glu Asp Pro Pro Gly Glu
56  65                  70                  75                  80
58 gag gat cta cct gga gag gag gat cta cct gga gag gag gat cta cct   288
59 Glu Asp Leu Pro Gly Glu Glu Asp Leu Pro Gly Glu Glu Asp Leu Pro
60                  85                  90                  95
62 gaa gtt aag cct aaa tca gaa gaa gag ggc tcc ctg aag tta gag gat   336
```

```
63 Glu Val Lys Pro Lys Ser Glu Glu Glu Gly Ser Leu Lys Leu Glu Asp
64             100                 105                 110
66 cta cct act gtt gag gct cct gga gat cct caa gaa ccc cag aat aat      384
67 Leu Pro Thr Val Glu Ala Pro Gly Asp Pro Gln Glu Pro Gln Asn Asn
68             115                 120                 125
70 gcc cac agg gac aaa gaa ggg gat gac cag agt cat tgg cgc tat gga      432
71 Ala His Arg Asp Lys Glu Gly Asp Asp Gln Ser His Trp Arg Tyr Gly
72         130                 135                 140
74 ggc gac ccg ccc tgg ccc cgg gtg tcc cca gcc tgc gcg ggc cgc ttc      480
75 Gly Asp Pro Pro Trp Pro Arg Val Ser Pro Ala Cys Ala Gly Arg Phe
76 145                 150                 155                 160
78 cag tcc ccg gtg gat atc cgc ccc cag ctc gcc gcc ttc tgc ccg gcc      528
79 Gln Ser Pro Val Asp Ile Arg Pro Gln Leu Ala Ala Phe Cys Pro Ala
80                 165                 170                 175
82 ctg cgc ccc ctg gaa ctc ctg ggc ttc cag ctc ccg ccg ctc cca gaa      576
83 Leu Arg Pro Leu Glu Leu Leu Gly Phe Gln Leu Pro Pro Leu Pro Glu
84             180                 185                 190
86 ctg cgc ctg cgc aac aat ggc cac agt gtg caa ctg acc ctg cct cct      624
87 Leu Arg Leu Arg Asn Asn Gly His Ser Val Gln Leu Thr Leu Pro Pro
88             195                 200                 205
90 ggg cta gag atg gct ctg ggt ccc ggg cgg gag tac cgg gct ctg cag      672
91 Gly Leu Glu Met Ala Leu Gly Pro Gly Arg Glu Tyr Arg Ala Leu Gln
92         210                 215                 220
94 ctg cat ctg cac tgg ggg gct gca ggt cgt ccg ggc tcg gag cac act      720
95 Leu His Leu His Trp Gly Ala Ala Gly Arg Pro Gly Ser Glu His Thr
96 225                 230         .            235                 240
98 gtg gaa ggc cac cgt ttc cct gcc gag atc cac gtg gtt cac ctc agc      768
99 Val Glu Gly His Arg Phe Pro Ala Glu Ile His Val Val His Leu Ser
100                 245                 250                 255
102 acc gcc ttt gcc aga gtt gac gag gcc ttg ggg cgc ccg gga ggc ctg     816
103 Thr Ala Phe Ala Arg Val Asp Glu Ala Leu Gly Arg Pro Gly Gly Leu
104             260                 265                 270
106 gcc gtg ttg gcc gcc ttt ctg gag gag ggc ccg gaa gaa aac agt gcc     864
107 Ala Val Leu Ala Ala Phe Leu Glu Glu Gly Pro Glu Glu Asn Ser Ala
108             275                 280                 285
110 tat gag cag ttg ctg tct cgc ttg gaa gaa atc gct gag gaa ggc tca     912
111 Tyr Glu Gln Leu Leu Ser Arg Leu Glu Glu Ile Ala Glu Glu Gly Ser
112         290                 295                 300
114 gag act cag gtc cca gga ctg gac ata tct gca ctc ctg ccc tct gac     960
115 Glu Thr Gln Val Pro Gly Leu Asp Ile Ser Ala Leu Leu Pro Ser Asp
116 305                 310                 315                 320
118 ttc agc cgc tac ttc caa tat gag ggg tct ctg act aca ccg ccc tgt     1008
119 Phe Ser Arg Tyr Phe Gln Tyr Glu Gly Ser Leu Thr Thr Pro Pro Cys
120                 325                 330                 . 335
123 gcc cag ggt gtc atc tgg act gtg ttt aac cag aca gtg atg ctg agt     1056
124 Ala Gln Gly Val Ile Trp Thr Val Phe Asn Gln Thr Val Met Leu Ser
125             340                 345                 350
127 gct aag cag ctc cac acc ctc tct gac acc ctg tgg gga cct ggt gac     1104
128 Ala Lys Gln Leu His Thr Leu Ser Asp Thr Leu Trp Gly Pro Gly Asp
```

```
129          355                   360                   365
131 tct cgg cta cag ctg aac ttc cga gcg acg cag cct ttg aat ggg cga    1152
132 Ser Arg Leu Gln Leu Asn Phe Arg Ala Thr Gln Pro Leu Asn Gly Arg
133      370                   375                   380
135 gtg att gag gcc tcc ttc cct gct gga gtg gac agc agt cct cgg gct    1200
136 Val Ile Glu Ala Ser Phe Pro Ala Gly Val Asp Ser Ser Pro Arg Ala
137 385                   390                   395                   400
139 gct gag cca gtc cag ctg aat tcc tgc ctg gct gct ggt gac atc cta    1248
140 Ala Glu Pro Val Gln Leu Asn Ser Cys Leu Ala Ala Gly Asp Ile Leu
141                   405                   410                   415
143 gcc ctg gtt ttt ggc ctc ctt ttt gct gtc acc agc gtc gcg ttc ctt    1296
144 Ala Leu Val Phe Gly Leu Leu Phe Ala Val Thr Ser Val Ala Phe Leu
145                   420                   425                   430
147 gtg cag atg aga agg cag cac aga agg gga acc aaa ggg ggt gtg agc    1344
148 Val Gln Met Arg Arg Gln His Arg Arg Gly Thr Lys Gly Gly Val Ser
149          435                   440                   445
151 tac cgc cca gca gag gta gcc gag act gga gcc tag                      1380
152 Tyr Arg Pro Ala Glu Val Ala Glu Thr Gly Ala  *
153      450                   455
156 <210> SEQ ID NO: 2
157 <211> LENGTH: 459
158 <212> TYPE: PRT
159 <213> ORGANISM: Homo sapiens
161 <400> SEQUENCE: 2
162 Met Ala Pro Leu Cys Pro Ser Pro Trp Leu Pro Leu Leu Ile Pro Ala
163 1               5                   10                  15
164 Pro Ala Pro Gly Leu Thr Val Gln Leu Leu Leu Ser Leu Leu Leu Leu
165              20                  25                  30
166 Met Pro Val His Pro Gln Arg Leu Pro Arg Met Gln Glu Asp Ser Pro
167          35                  40                  45
168 Leu Gly Gly Gly Ser Ser Gly Glu Asp Asp Pro Leu Gly Glu Glu Asp
169      50                  55                  60
170 Leu Pro Ser Glu Glu Asp Ser Pro Arg Glu Glu Asp Pro Pro Gly Glu
171 65                  70                  75                  80
172 Glu Asp Leu Pro Gly Glu Glu Asp Leu Pro Gly Glu Glu Asp Leu Pro
173              85                  90                  95
174 Glu Val Lys Pro Lys Ser Glu Glu Glu Gly Ser Leu Lys Leu Glu Asp
175              100                 105                 110
176 Leu Pro Thr Val Glu Ala Pro Gly Asp Pro Gln Glu Pro Gln Asn Asn
177          115                 120                 125
178 Ala His Arg Asp Lys Glu Gly Asp Asp Gln Ser His Trp Arg Tyr Gly
179      130                 135                 140
180 Gly Asp Pro Pro Trp Pro Arg Val Ser Pro Ala Cys Ala Gly Arg Phe
181 145                 150                 155                 160
182 Gln Ser Pro Val Asp Ile Arg Pro Gln Leu Ala Ala Phe Cys Pro Ala
183              165                 170                 175
184 Leu Arg Pro Leu Glu Leu Leu Gly Phe Gln Leu Pro Pro Leu Pro Glu
185              180                 185                 190
186 Leu Arg Leu Arg Asn Asn Gly His Ser Val Gln Leu Thr Leu Pro Pro
```

```
187           195                 200                 205
188 Gly Leu Glu Met Ala Leu Gly Pro Gly Arg Glu Tyr Arg Ala Leu Gln
189     210                 215             220
190 Leu His Leu His Trp Gly Ala Ala Gly Arg Pro Gly Ser Glu His Thr
191 225                 230                 235                 240
192 Val Glu Gly His Arg Phe Pro Ala Glu Ile His Val Val His Leu Ser
193                 245                 250                 255
194 Thr Ala Phe Ala Arg Val Asp Glu Ala Leu Gly Arg Pro Gly Gly Leu
195             260                 265                 270
196 Ala Val Leu Ala Ala Phe Leu Glu Glu Gly Pro Glu Glu Asn Ser Ala
197         275                 280                 285
198 Tyr Glu Gln Leu Leu Ser Arg Leu Glu Glu Ile Ala Glu Glu Gly Ser
199     290                 295                 300
200 Glu Thr Gln Val Pro Gly Leu Asp Ile Ser Ala Leu Leu Pro Ser Asp
201 305                 310                 315                 320
202 Phe Ser Arg Tyr Phe Gln Tyr Glu Gly Ser Leu Thr Thr Pro Pro Cys
203                 325                 330                 335
204 Ala Gln Gly Val Ile Trp Thr Val Phe Asn Gln Thr Val Met Leu Ser
205             340                 345                 350
206 Ala Lys Gln Leu His Thr Leu Ser Asp Thr Leu Trp Gly Pro Gly Asp
207         355                 360                 365
208 Ser Arg Leu Gln Leu Asn Phe Arg Ala Thr Gln Pro Leu Asn Gly Arg
209     370                 375                 380
210 Val Ile Glu Ala Ser Phe Pro Ala Gly Val Asp Ser Ser Pro Arg Ala
211 385                 390                 395                 400
212 Ala Glu Pro Val Gln Leu Asn Ser Cys Leu Ala Ala Gly Asp Ile Leu
213                 405                 410                 415
214 Ala Leu Val Phe Gly Leu Leu Phe Ala Val Thr Ser Val Ala Phe Leu
215             420                 425                 430
216 Val Gln Met Arg Arg Gln His Arg Arg Gly Thr Lys Gly Gly Val Ser
217         435                 440                 445
218 Tyr Arg Pro Ala Glu Val Ala Glu Thr Gly Ala
219     450                 455
222 <210> SEQ ID NO: 3
223 <211> LENGTH: 540
224 <212> TYPE: DNA
225 <213> ORGANISM: Artificial Sequence
227 <220> FEATURE:
228 <223> OTHER INFORMATION: Coding sequence for human CA IX proteoglycan
229       domain construct
```

W--> `231 <221> NAME/KEY: CDS`

```
232 <222> LOCATION: (1)...(540)
```

W--> `237 <400> 3`

```
238 atg gct ccc ctg tgc ccc agc ccc tgg ctc cct ctg ttg atc ccg gcc    48
239 Met Ala Pro Leu Cys Pro Ser Pro Trp Leu Pro Leu Leu Ile Pro Ala
240 1               5                   10                  15
242 ctt gct cca ggc ctc act gtg caa ctg ctg ctg tca ctg ctg ctt ctg    96
243 Leu Ala Pro Gly Leu Thr Val Gln Leu Leu Leu Ser Leu Leu Leu Leu
244             20                  25                  30
```

RAW SEQUENCE LISTING   DATE: 03/08/2007
PATENT APPLICATION: US/10/525,535   TIME: 14:57:10

Input Set : N:\efs\03_08_07\10525535_efs\324503SequenceListing.txt
Output Set: N:\CRF4\03082007\J525535.raw

```
246 atg cct gtc cat ccc cag agg ttg ccc cgg atg cag gag gat tcc ccc   144
247 Met Pro Val His Pro Gln Arg Leu Pro Arg Met Gln Glu Asp Ser Pro
248         35                  40                  45
250 ttg gga gga ggc tct tct ggg gaa gat gac cca ctg ggc gag gag gat   192
251 Leu Gly Gly Gly Ser Ser Gly Glu Asp Asp Pro Leu Gly Glu Glu Asp
252         50                  55                  60
254 ctg ccc agt gaa gag gat tca ccc aga gag gag gat cca ccc gga gag   240
255 Leu Pro Ser Glu Glu Asp Ser Pro Arg Glu Glu Asp Pro Pro Gly Glu
256   65                  70                  75                  80
258 gag gat cta cct gga gag gag gat cta cct gga gag gag gat cta cct   288
259 Glu Asp Leu Pro Gly Glu Glu Asp Leu Pro Gly Glu Glu Asp Leu Pro
260                 85                  90                  95
262 gaa gtt aag cct aaa tca gaa gaa gag ggc tcc ctg aag tta gag gat   336
263 Glu Val Lys Pro Lys Ser Glu Glu Glu Gly Ser Leu Lys Leu Glu Asp
264             100                 105                 110
266 cta cct act gtt gag gct cct gga gat cct caa gaa ccc cag aat aat   384
267 Leu Pro Thr Val Glu Ala Pro Gly Asp Pro Gln Glu Pro Gln Asn Asn
268         115                 120                 125
270 gcc cat agg agc tcg agc atc cta gcc ctg gtt ttt ggc ctc ctt ttt   432
271 Ala His Arg Ser Ser Ser Ile Leu Ala Leu Val Phe Gly Leu Leu Phe
272         130                 135                 140
274 gct gtc acc agc gtc gcg ttc ctt gtg cag atg aga agg cag cac aga   480
275 Ala Val Thr Ser Val Ala Phe Leu Val Gln Met Arg Arg Gln His Arg
276 145                 150                 155                 160
278 agg gga acc aaa ggg ggt gtg agc tac cgc cca gca gag gta gcc gag   528
279 Arg Gly Thr Lys Gly Gly Val Ser Tyr Arg Pro Ala Glu Val Ala Glu
280             165                 170                 175
282 act gga gcc tag                                                   540
283 Thr Gly Ala   *
287 <210> SEQ ID NO: 4
288 <211> LENGTH: 179
289 <212> TYPE: PRT
290 <213> ORGANISM: Artifical Sequence
292 <220> FEATURE:
294 <223> OTHER INFORMATION: Polypeptide encoded by coding sequence for human
295      CA IX proteoglycan domain construct
297 <400> SEQUENCE: 4
298 Met Ala Pro Leu Cys Pro Ser Pro Trp Leu Pro Leu Leu Ile Pro Ala
299 1               5                   10                  15
300 Leu Ala Pro Gly Leu Thr Val Gln Leu Leu Leu Ser Leu Leu Leu Leu
301             20                  25                  30
302 Met Pro Val His Pro Gln Arg Leu Pro Arg Met Gln Glu Asp Ser Pro
303         35                  40                  45
304 Leu Gly Gly Gly Ser Ser Gly Glu Asp Asp Pro Leu Gly Glu Glu Asp
305         50                  55                  60
306 Leu Pro Ser Glu Glu Asp Ser Pro Arg Glu Glu Asp Pro Pro Gly Glu
307 65                  70                  75                  80
308 Glu Asp Leu Pro Gly Glu Glu Asp Leu Pro Gly Glu Glu Asp Leu Pro
309                 85                  90                  95
```

C--> 290 `<213> ORGANISM: Artifical Sequence`

VERIFICATION SUMMARY   DATE: 03/08/2007
PATENT APPLICATION: US/10/525,535   TIME: 14:57:11

Input Set : **N:\efs\03_08_07\10525535_efs\324503SequenceListing.txt**
Output Set: **N:\CRF4\03082007\J525535.raw**

```
L:231 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:237 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3
L:290 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:4
L:333 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:336 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:5
L:500 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:503 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:7
L:657 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:660 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:9
```